Cross-talk between the Notch and TGF-β signaling pathways mediated by interaction of the Notch intracellular domain with Smad3

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The Notch and TGF-β signaling pathways play critical roles in the control of cell fate during metazoan development. However, mechanisms of cross-talk and signal integration between the two systems are unknown. Here, we demonstrate a functional synergism between Notch and TGF-β signaling in the regulation of Hes-1, a direct target of the Notch pathway. Activation of TGF-β signaling up-regulated Hes-1 expression in vitro and in vivo. This effect was abrogated in myogenic cells by a dominant-negative form of CSL, an essential DNA-binding component of the Notch pathway. TGF-β regulated transcription from the Hes-1 promoter in a Notch-dependent manner, and the intracellular domain of Notch1 (NICD) cooperated synergistically with Smad3, an intracellular transducer of TGF-β signals, to induce the activation of synthetic promoters containing multimerized CSL- or Smad3-binding sites. NICD and Smad3 were shown to interact directly, both in vitro and in cells, in a ligand-dependent manner, and Smad3 could be recruited to CSL-binding sites on DNA in the presence of CSL and NICD. These findings indicate that Notch and TGF-β signals are integrated by direct protein-protein interactions between the signal-transducing intracellular elements from both pathways.

Introduction

The Notch and TGF-β signaling pathways are important for the control of cellular differentiation and display principal similarities in their mode of signaling (for review see Artavanis-Tsakonas et al., 1999; Massagué et al., 2000). As summarized in Fig. 1 A, the ligand-induced signal is in both cases transmitted via membrane-proximal components, i.e., the Notch intracellular domain (NICD) and Smads, respectively, which relocate from the cytoplasm to the nucleus to control gene activation. Binding of TGF-β to type I and II serine-threonine kinase receptors results in phosphorylation and dissociation of receptor-regulated Smads. This group of Smad proteins is ligand-specific, i.e., Smads 1, 5, and 8 mediate bone morphogenetic protein signaling, whereas Smad2 and 3 participate in TGF-β and activin signaling. Smad4 is an essential signaling component common to all TGF-β superfamily ligands that associates with phosphorylated receptor-regulated Smads. In the nucleus, the complex of receptor-regulated Smads and Smad4 cooperates with additional coactivators, corepressors, and tissue-specific factors to regulate transcription of target genes (Attisano and Wrana, 2002). Activation of Notch by cell-bound ligands (Delta or Serrate) results in proteolytic cleavage of the NICD and its translocation to the cell nucleus, where it is recruited to target genes via interaction with CSL (RBP-Jk/CBF1), an essential DNA-binding component of the Notch pathway (for review see Artavanis-Tsakonas et al., 1999).

Notch and TGF-β signaling converge in the regulation of a number of developmental processes, including myogenic, endothelial, pancreatic, and neuronal differentiation. However, it is at present assumed that the two systems act in parallel, largely independent pathways to regulate expression of target genes. A recent microarray survey of transcriptional changes in human keratinocytes exposed to TGF-β identified several components of the Notch pathway, including the basic helix-loop-helix transcription factor Hes-1, a direct target of

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Abbreviations used in this paper: E, embryonic day; NICD, Notch intracellular domain.

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Results and discussion

Electroporation of a constitutively active form of the type I TGF-β receptor (CA-ALK5) in the precardial mesoderm of embryonic day 2 (E2) chicken embryos resulted in ectopic expression of the chick Hes-1 homologue c-hairy in the heart at E4 (Fig. 1 B). In no case was ectopic expression of c-hairy detected after electroporation of a control construct (Fig. 1 B). Electroporation of CA-ALK5 in the mesencephalic vesicle resulted in a 2.3-fold increase in c-hairy expression in the midbrain, as evaluated by real-time PCR analysis of electroporated tissue (Fig. 1 C). Stimulation of adult neural stem cells and C2C12 myoblasts with TGF-β induced a rapid (<60 min) increase in Hes-1 expression in both cell types (Fig. 1, D and E). Blockade of protein translation by prior treatment of C2C12 cells with cycloheximide did not affect induction of Hes-1 expression by TGF-β (Fig. 1 E), indicating that Hes-1 is a direct target of TGF-β signaling.

The requirement of Notch signaling was tested by transfecting C2C12 cells with a GFP expression plasmid and a dominant-negative CSL construct carrying a point mutation (R218H) that renders it unable to interact with DNA, and that has been shown to effectively block Notch signaling in other systems (Wettstein et al., 1997). CSL R281H abolished the effects of TGF-β on Hes-1 expression in GFP-positive cells isolated by cell sorting (Fig. 2 A), indicating the involvement of endogenous Notch signaling. Induction of PAI-1, a classical target of the TGF-β pathway, was unaffected by CSL R281H (Fig. 2 A). In addition, TGF-β stimulated transcription from a reporter construct containing 500 bp of upstream sequence from the Hes-1 promoter in C2C12 cells overexpressing NICD (Fig. 2 B), in agreement with a synergistic interaction between the two pathways.

TGF-β augmented transcriptional activity from a reporter construct carrying multimerized CSL-binding sites (12xCSL-luc; Wallberg et al., 2002) in C2C12 myoblasts and C17.2 neural stem cells overexpressing NICD (Fig. 3, A and B). In the absence of NICD, overexpression
of Smad proteins had no effect on the activity of the 12xCSL-luc reporter. However, in the presence of NICD, Smad3 increased the relative responsiveness of the 12xCSL-luc reporter to TGF-β (Fig. 3, A and B), indicating a synergistic cooperation of the two factors to regulate ligand-dependent gene transcription. Despite the inability of overexpressed Smad4 to potentiate NICD activity in C2C12 cells (Fig. 3, A and B), TGF-β failed to enhance NICD-mediated 12xCSL-luc activity in a human breast cancer cell line (MDA468) that lacks a functional Smad4 protein (Schutte et al., 1996; Fig. 3 C). Ligand-dependent activation of 12xCSL-luc could be restored upon transfection of Smad3 together with Smad4, but not Smad3 alone (Fig. 3 C), suggesting that Smad3 is nevertheless required for the functional interaction between the Notch and TGF-β signaling pathways. A point mutant of Smad3 that is unable to bind DNA (K81R Smad3; Morén et al., 2000) could not enhance basal 12xCSL-luc activity (Chapman, G., personal communication)—higher levels of endogenous Smad3 may not need to bind DNA directly in order to cooperate with NICD to regulate gene transcription.

Next, we used a Gal4–NICD fusion construct, which bypasses the requirement of CSL for the recruitment of NICD to DNA (Beatus et al., 2001), together with a reporter construct carrying a multimerized Gal4-binding site (MH100, herein referred to as Gal4-luc). Transfection of Gal4–NICD activated this reporter, and this effect could be potentiated by cotransfection of Smad3 (Fig. 3 D), which on its own had no effect on the activity of the Gal4-luc reporter (unpublished data). These data suggested that a synergistic interaction between the Notch and TGF-β signaling pathways may take place even in the absence of CSL, as long as NICD and Smad3 (and presumably also Smad4) are present. We also used a reporter construct carrying nine tandem copies of the Smad-binding element from the PAI-1 promoter (CAGA-luc) that is specific for Smad3 and highly responsive to TGF-β (Dennler et al., 1998). Although largely insensitive to NICD in the absence of TGF-β, the transcriptional activity of this reporter in response to TGF-β could be further enhanced by NICD in a dose-dependent manner (Fig. 3 E).

The possibility that NICD and Smad3 may be able to interact directly was first investigated in vitro using GST–Smad fusion proteins produced in bacteria and 35S-labeled NICD produced by in vitro translation. A GST fusion of full-length Smad3, but not of Smad1, Smad4, or GST alone, was able to pull down 35S-labeled NICD (Fig. 4 A), indicating that Smad3 and NICD have the capacity of interacting with each other in the absence of additional components. In mammalian cells expressing myc-tagged NICD and Flag-tagged Smad3, immunoprecipitation with anti-Flag antibodies allowed the recovery of myc-tagged NICD only from extracts of cells that had also received the Flag–Smad3 construct (Fig. 4 B). It was also capable of potentiating the response of the 12xCSL-luc reporter to Notch and TGF-β signaling (Fig. 3, A and B), suggesting that Smad3 may not need to bind DNA directly in order to cooperate with NICD to regulate gene transcription.
could be recovered in Notch1 immunoprecipitates (Fig. 5 A). Importantly, this interaction could be further enhanced by treatment with TGF-β (Fig. 5 A), demonstrating a ligand-dependent association between Smad3 and Notch in myoblast cells.

Finally, we used a biotinylated oligonucleotide containing two tandem CSL-binding sites to probe combinations of GST–Smad3 and in vitro–translated NICD and CSL in a cell-free system. GST–Smad3 could only be precipitated by the biotinylated oligonucleotide in the presence of both NICD and CSL, but not NICD or CSL alone (Fig. 5 B), indicating that Smad3 depends on its ability to interact with NICD for its recruitment to CSL DNA-binding sites. Importantly, a mutated oligonucleotide carrying three point mutations in the consensus site of CSL binding was unable to recover GST–Smad3 under any condition (Fig. 5 B), underlying the specificity of these protein–DNA interactions.

Together, these results suggest that Smad3 can be recruited to the promoter regions of Notch target genes via direct interaction with NICD (Fig. 5 C). In a reciprocal situation, our observations suggest a mechanism by which Notch signaling could influence the expression of TGF-β target genes. Although previous work has revealed several examples of cross-regulatory interactions between Notch and other pathways, including Wnt (Espinosa et al., 2003) and Ras (Shaye and Greenwald, 2002), Notch signaling had until now not been shown to be involved in a direct cross-talk mediated by defined protein–protein interactions with signaling components from other major ligand systems.

Notch signaling profoundly influences the differentiation of many cell types, and there are several situations in which Notch and TGF-β signaling are known to converge. During myogenesis, induction of Hes-1 by Notch inhibits the expression of myogenic regulatory factors, such as the basic helix-loop-helix transcription factor MyoD (Kuroda et al., 1999). TGF-β signaling also inhibits myogenesis, induction of muscle-specific gene expression, and myotube formation in cultured myoblasts without affecting cell proliferation (Massagué et al., 1986). Although Smad3 has
been shown to repress the activity of MyoD through direct protein–protein interactions (Liu et al., 2001), the results presented here highlight a more upstream point of convergence between the two pathways. Notch and TGF-β signaling are also known to converge in the regulation of several other differentiation events, for example during endothelial (Goumans et al., 2002), pancreas (Kim and Hebrok, 2001), and neural (Shah et al., 1996) development. Our findings indicate an unexpected level of cross-talk between two major signaling pathways, and warrant further investigations on the roles of Smad3–NICD interactions in the coordination of metazoan development.

Materials and methods

In ovo electroporation of chicken embryos

Embryos from fertilized white leghorn eggs were electroporated at Hamberg and Hamilton (HH) stages 8–10 (~E2) with constructs at a final concentration of 0.4 μg/ml in the presence of 0.4 μg/ml EGFP (CLONTECH Laboratories, Inc.) in 1× PBS and 0.2% Fast Green using an Electro-Square Porator (model ECM830; Genetronics, Inc.) at 20 V with five pulses of 13 ms. Stage 8–9 embryos were used for targeting the precardin mesoderm in the vicinity of the cephalic mesenchyme, whereas stage 10 embryos were injected in the mesencephalic vesicle for analysis of brain expression. 2 d after electroporation (HH stages 21–23), surviving embryos with the appropriate targeting of GFP expression (i.e., heart or brain) were subjected to either whole-mount in situ hybridization (heart) or real-time PCR (brain) for analysis of c-hairy mRNA expression. Chick embryos were photographed with a digital camera (Kodak) mounted to a dissection microscope (Carl Zeiss Microimaging, Inc.) at 2×.

In situ hybridization and real-time PCR

Whole-mount in situ hybridization for c-hairy expression was performed according to previously published procedures (Palmeirim et al., 1997), but omitting proteinase K digestion. 1 d after transfection, C2C12 cells were mechanically detached from the plate, and GFP-positive cells were sorted by FACS® analysis in a FACSvantagentTM SE System (Becton Dickinson). GFP-positive cells were cultured for another 24 h and then treated with TGF-β for 60 min before RNA isolation and cDNA synthesis. Real-time PCR was performed in a LightCycler system (PerkinElmer). PCR primer sequences are available on request. All results are expressed relative to GADPH values obtained in parallel reactions.

Plasmid constructs, cell transfection, and reporter assays

The Hes-1 reporter construct contains 0.5 kb of upstream sequence of the Hes-1 gene followed by a luciferase reporter (Jarraiut et al., 1995). The 12xCSL-luc reporter contains a hexameric 50-bp repeat of the EBNA2 response element of the TP-1 promoter (Dennler et al., 1998). All Smad expression plasmids have been described elsewhere (Morén et al., 2000). The NICS constructs used for reporter and pull-down assays were derived from the intracellular domain of the mouse Notch1 receptor (Kopan et al., 1994; Beatus et al., 2001; Wallberg et al., 2002). COS cells were transfected by the calcium phosphate method. C2C12, MDA468, and C17.2 cells were transfected in complete medium with FuGene™ 6 (Roche). After 24 h incubation, cell monolayers were washed with serum-free medium and incubated for a further 16 h in 0.1% serum-containing medium supplemented with 10 ng/ml TGF-β1 or 40 ng/ml BMP-4 (R&D Systems) as indicated. Cycloheximide (Sigma-Aldrich) was used at 25 μg/ml. Reporter assays were performed and analyzed as described previously (Blokkzijl et al., 2002). All treatments and transcription conditions were analyzed in triplicate.

Pull-down and coimmunoprecipitation assays

GST fusions were produced in Escherichia coli and purified by chromatography on glutathione–agarose beads (Amersham Biosciences). In vitro–translated products were produced using a kit from Promega. Anti-Flag mAb was from Kodak or Sigma-Aldrich, anti-myc 9E1 mAb was from Covance or BD Biosciences. Cell lysates and immunoprecipitations were done as described previously (Blokkzijl et al., 2002). Parental and Notch1–transfected C2C12 cells were starved in serum-free medium for 4 h before treatment with 10 ng/ml TGF-β1 for 50 min. Triton X-100 cell lysates were immunoprecipitated with anti-Notch1 antibodies (M-20; Santa Cruz Biotechnology, Inc.) that had previously been covalently coupled to CNBr-activated Sepharose beads (Amersham Biosciences). Immunoblots were probed with an anti-Smad3 pAb (Zymed Laboratories). Oligonucleotide pull-down assays were performed with biotinylated 50-mer oligonucleotides containing the EBNA2 response element of the TP-1 promoter (equivalent to two CSL-binding sites) with sequence as follows: 5’T-GATCCCCACGTGGGAAATGGCGGAGGCGAAGGGCACCGTGGAAGAAGAG-3’TAGTA-3’ (mutations in bold). Different combinations of GST–Smad3, 35S-labeled NICD, and 35S-labeled CSL produced as above were mixed 1:1 with H buffer (20 mM Heps, 50 mM KCl, 20% glycerol, 0.1% NP-40, and 1 mM DTT) plus biotinylated oligonucleotide and polyvaldC (50 μg/ml). After 2 h at 4°C, streptavidin beads (Pierce Chemical Co.) were added, followed by an additional 1 h of incubation, precipitation, and washing in H buffer with additional salt (up to 300 mM). Immunoblots were processed by autoradiography and subsequently probed with anti-GST antibodies to detect GST-tagged Smad3.

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